VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Please amend the paragraph beginning on page 16, line 16 and continuing to page 17, line 7 as follows:

Only allelic variants of the GCT10D04 locus (primers; SCZ15:GGGGCAGCGGGTCCAGAATCTTC (SEQ. ID NO: 3), SCZ16: TCGCCTTGCTGCCCGTAGTGCT (SEQ. ID NO: 11); annealing temperature 62°C) showed an overall significant group effect for the L allele (Kruskal-Wallis H (2, N= 194) = 12.18, p = .002); the CAG repeat average length being the shortest in the neuroleptic-responders (Rs), intermediate in the non-responders (NRs) and longest in the control group (C) (Fig. 1).

IN THE CLAIMS:

1. (Amended) [A] An isolated human hGT1 gene [containing] comprising a transcribed polymorphic CAG repeat [, which comprises a sequence as set forth in Fig. 3 and Figs. 4A-4C,] having the sequence $(CAU)_2(CAG)_nCAA$, wherein U is A or G and n is from 7 to 12, wherein allelic variants of said CAG repeat are associated with a disorder selected from the group consisting of [alleles -3, -2, -1, 0 and 1, and wherein said allelic variants are associated with] psychiatric diseases, schizophrenia, affective disorders, neurodevelopmental brain diseases and [or with] phenotypic variability with respect to long term response to neuroleptic medication, and wherein n being equal to 11 is the most common allele of the hGT1 gene.

3. (Amended) A method for evaluating the [prognosis of] severity of schizophrenia of a patient, which comprises the steps of:

a) obtaining a nucleic acid sample of said patient; and

b) determining allelic variants of said CAG repeat of the gene of claim 1, [and]

wherein allelic variants shorter than allele 0, which corresponds to n=11, are indicative of [non-severe schizophrenia] less severe schizophrenia in the patient.

4. (Amended) A method for the identification of the response of a patient [responding] to neuroleptic medication, which comprises the steps of:

a) obtaining a nucleic acid sample of said patient; and

b) determining allelic variants of said CAG repeat of the gene of claim 1, [and]

wherein allelic variants shorter than allele 0, which corresponds to n=11, are indicative of a neuroleptic response by said patient.

5. (Amended) The method of claim 4, wherein said shorter allelic variants have [from about 171 to about 177 bp in length] a n equal to 8, 9 or 10.

9. (Amended) A method of categorizing a psychiatric patient[s] according to [their] its genotype in order to maximize its response to treatment [patients] to at least one neuroleptic drug, which comprises the steps of:

a) obtaining a nucleic acid sample of said patient[s]; and

b) determining allelic variants of said CAG repeat of the gene of claim 1,

wherein a patient is [patients are] categorized with respect to [their] his allelic variants, and wherein allelic variants shorter than allele 0, which corresponds to n=11, are indicative of a neuroleptic response of said patient.

10. (Amended) [The use of the determination of] A method of identifying a patient which is responsive to a neuroleptic medication which comprises:

a) obtaining a sample from said patient; and

b) determining allelic variants of said CAG repeat of the gene of claim 1 [for the identification of patient responding to neuroleptic medication],

wherein allelic variants shorter than allele 0, which corresponds to n=11, identify said patient as a neuroleptic responder [are indicative of neuroleptic response].

11. (Amended) The [use] method of claim 10, wherein said sample is a nucleic acid sample and wherein shorter allelic variants have a n equal to 8, 9 or 10 [from about 171 to about 177 bp in length].

ABSTRACT

The hGT1 gene is a polymorphic CAG repeat-containing gene. Uses of the hGT1 gene include the diagnosis, predictive prognosis and treatment of psychiatric diseases, such as schizophrenia.